

1 GCCCCACCACGCCCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTGGAGGCCAAG 60
 CGGGGTGGTGCAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCA
 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys

 61 GAGGCCGAGAATATCACGACGGCTGTGCTGAACACTGCAGCTGAATGAGAATATCACT 120
 CTCCGGCTTATAGTGCTGCCGACACGACTTGTGACGTCGAACCTACTCTTATAGTGA
 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr

 121 GTCCCAGACACCAAAGTTAATTCTATGCCCTGGAAGAGGATGGAGGTCGGCAGCAGGCC 180
 CAGGGTCTGTGGTTCAATTAAAGATACGGACCTCTCCTACCTCCAGCCCGTCCGG
 ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla

 181 GTAGAACGCTGGCAGGGCTGGCCCTGCTGCGGAAGCTGTCCTGCGGGGCCAGGCCCTG 240
 CATCTTCAGACCGTCCGGACCGGACAGCAGCCTCGACAGGACGCCCGTCCGG
 ValGluValTrpGlnGlyLeuAlaLeuSerGluAlaValLeuArgGlyGlnAlaLeu

 241 TTGGTCAACTCTTCCCAGCCGTGGAGCCCTGCAGCTGCATGTGGATAAGCCGTCAGT 300
 AACCAAGTTGAGAAGGGTCGGCACCCCTCGGGGACGTCGACGTACACCTATTCCGGCAGTCA
 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer

 301 GGCCTTCGCAGCCTCACCACTCTGCTTCGGCTCTGGAGCCAGAAGGAAGCCATCTCC 360
 CCGGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCTCGGGTCTTCCTTCGGTAGAGG
 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer

 361 CCTCCAGATGCGGCCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTCCGAAA 420
 GGAGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTAGTGACGACTGTGAAAGGCCTT
 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys

 421 CTCTCCGAGTCTACTCCAATTCCCTCGGGAAAGCTGAAGCTGTACACAGGGGAGGCC 480
 GAGAAGGCTCAGATGAGGTTAAAGGAGGCCCTTCGACTTCGACATGTGTCCTCCGG
 LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla

 TGCAGGACAGGGGACAGATGA (SEQ ID NO:120)
 481 -----+-----+ 501
 ACGTCCTGTCCCCTGTCTACT (SEQ ID NO:135)
 CysArgThrGlyAspArg (SEQ ID NO:121)

Figure 5